SEQUENCE LISTING

	ľ	
5	(1) GENERAL INFORMATION:	
10	i) APPLICANT: (A) NAME: Zeneca MOGEN (B) STREET: Einsteinweg 97 (C) CITY: Leiden (E) COUNTRY: The Netherlands (F) POSTAL CODE (ZIP): 2333 CB (G) TELEPHONE: (31) 71-5258282	
15	(H) TELEFAX: (31) 71-5221471	
	(ii) TITLE OF INVENTION: New constitutive plant promoters	
	(iii) NUMBER OF SEQUENCES: 22	
20	<pre>(iv) COMPUTER READABLE FORM: (A) MEDIUM TYPE: Floppy disk (B) COMPUTER: IBM PC compatible (C) OPERATING SYSTEM: PC-DOS/MS-DOS (D) SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)</pre>	
25		
••	(vi) PRIOR APPLICATION DATA: (A) APPLICATION NUMBER: EP 97203912.7 (B) FILING DATE: 12-DEC-1997	
30	(2) INFORMATION FOR SEQ ID NO. 1:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 520 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic	
40	(iii) HYPOTHETICAL: NO	
45	(iii) ANTI-SENSE: NO	
43	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:	
	GACTGAAGTG TGAAGGTGGA GATTATGTAT TCACTTGTTO ATTTGGTATA CATTCTATGT	60
50	AAGGTŢCAAT TATTTACGTT ATATAATTAT AATGGAGTAA TTACAGTAA TTGGGTTAAA	120
	ATGGTTTGAT TCGGTCAGGT TGATACGGTT TGGAAGTTAA ACCCGGCCTA GATATGATGT	180
	TACAACCAGT CCACATCTTT TATGATTTTA GTGGAACAAA CGAGGTTA TTTAGACGAT	240
55	ACAAACAAGG TCCGAATAAG TGTGAGCTGT CCCAAGTAAG ACCACGTAAT ACTCACCTCA	300
	ACAAGATAGT GTTCTTAAAG TGTGTCAAAC ACAATCACAC ACACACAAAT CATAAAACAC	360
60	· AAAGACGATA ATCCATCGAT CCACAGAATA GACGCCACGT GGTAGAT	420
	AAAAGTTCTC ACCTTTTAAT CTTTCTCCAC GCCATTTCCA CAAGCCATAA TCCTCAAAAA	480
	TOTCAACTIT ATCTCCCAAA ACACAAATCT AGAAACCATG	520

The state of the s

WO 99/31258 PCT/EP98/08162

		(2) INFORMATION FOR SEQ ID NO: 2:	
	5	i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 300 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	10	(ii) MONECULE TYPE: DNA (genomic)	
		(iii) HYPOTHETICAL: NO	
		(iii) ANTI-SENSE: NO	
	15		
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:	
	20	CCCACTACAA TGAATTTGTT CGTGAACTAT TAGTTGCGGG CCTTGGCATC CGACTACCTC	60
		TGCGGCAATA TTATATTCCC TGGGCCCACC GTGAACCCAA TTTCGCCTAT TTATTCATTA	120
	-	CCCCCATTAA CATTGAAGTA GTCATGATGG GCCTGCAGCA CGTTGGTGAG GCTGGCACAA	180
1	25	CTCATCCATA TACTTTCTGA CCGGACGGC ACATTATTGT AGAAAACGCG GACCCACAGC	240
Seed them		GCACTITCCA AAGCGGTGCC GCGTCAGAAT GCGCTGGCAG AAAAAAATTA ATCCAAAAGT	300
	30	(2) INFORMATION FOR SEQ ID NO:	
Į.	35	(i) SEQUENCE CHARACTERISTICS (A) LENGTH: 840 base pairs	
= L		(B) TYPE: nucleic acid (C) STRANDEDNESS: double	
firm firm fluid		(D) TOPOLOGY: linear	
IJ		(ii) MOLECULE TYPE: DNA (genomic)	
	40	(iii) HYPOTHETICAL: NO	
		(iii) ANTI-SENSE: NO	
	45		
		(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:	
		GGATCCGAGC TTGCATGCCC CCACTACAAT GAATTTGTTC GTGAACTATT AGTTGCGGGC	60
	50	CTTGGCATCC GACTACCTCT GCGGCAATAT TATATTCCCT GGGCCCACCG TGAACCCAAT	120
		TTCGCCTATT TATTCATTAC CCCCATTAAC ATTGAAGTAG TCATGATGGG CCTGCAGCAC	180
	55	GTTGGTGAGG CTGGCACAAC TCATCCATAT ACTTTCTGAC CGGATCGGCA CATTATTGTA	300
		GAAAACGCGG ACCCACAGCG CACTTTCCAA AGCGGTGCCG CGTCAGAATG CGCTGGCAGA	360
	. 60	AAAAAATTAA TCCAAAAGTG ACTGAAGTGT GAAGGTGGAG ATTATGTATT CACTTGTTGA TTTGGTATAC ATTCTATGTA AGGTTCAATT ATTTACGTTA TATAATTATA A GGAGTAAT	420
	60	TTACAGTAAT TGGGTTAAAA TGGTTTGATT CGGTCAGGTT GATACGGTTT GGAAGTTAAA	480
		CCCGGCCTAG ATATGATGTT ACAACCAGTC CACATCTTTT ATGATTTAG TGGAACAAAC	540
	65	CCCGGCCIAG AIAIGAIGII ACAACCAGIC CACAICI.II AIGAIIIIAG IGGAACAAAC	541

3

29

AGATTTGTAT TGCAGCGATT TCATTTTAG

65

	(2) INFORMATION FOR SEQ ID NO: 6:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6: ATCTGGTCAC AGAGCTTGTC	20
20	(2) INFORMATION FOR SEQ ID NO: 7: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 25 base pairs (B) TYPE: nucleic acid	
25	(C) STRANDENESS: single (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: CDNA (iii) HYPOTHETICAL: NO	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7: GTCTCCATGG TGCTACAAAG AATAG	25
J.J	(2) INFORMATION FOR SEQ ID NO:\8:	25
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: cDNA	
50	(iii) HYPOTHETICAL: NO	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:	
	CGGGATCCTG CAGCGATTTC ATTTTAG	27
55	(2) INFORMATION FOR SEQ ID NO: 9:	
60	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
65	(iii) HYPOTHETICAL: NO	

```
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
5
                                                                              22
     ACATGAACGA ATGCAAAATC TC
     (2) INFORMATION FOR SEQ ID NO: 10:
10
          (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 22 base pairs
               (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
               (b) TOPOLOGY: linear
15
         (ii) MOLECULE TYPE: CDNA
        (iii) HYPOTRETICAL: NO
20
         (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
                                                                              22
     AGATTTTGCA TTCGTTCATG TG
25
     (2) INFORMATION FOR SEQ ID NO: 11:
          (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: \22 base pairs
30
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: \linear
         (11) MOLECULE TYPE: ODNA
35
         (iii) HYPOTHETICAL: NO
40
         (xi) SEQUENCE DESCRIPTION SEQ ID NO: 11:
                                                                               22
     TGTAAGCATT TCTTAGATTC TC
      (2) INFORMATION FOR SEQ ID NO: 12:
45
           (i) SEQUENCE CHARACTERISTICS
                (A) LENGTH: 22 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
50
                (D) TOPOLOGY: linear
          (ii) MOLECULE TYPE: cDNA
         (iii) HYPOTHETICAL: NO
 55
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
                                                                               22
 60
      AAGAAATGCT TACAGGATAT GG
      (2) INFORMATION FOR SEQ ID NO: 13:
           (i) SEQUENCE CHARACTERISTICS:
 65
                (A) LENGTH: 34 base pairs
```

	(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: CDNA	
,		
	(iii) HYPOTHETICAL: NO	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:	
	GACAAGCTTG ATCCCATGGT GCTACAAAGA ATAG	34
15	(2) INFORMATION FOR SEQ ID NO: 14:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LÀNGTH: 31 base pairs (B) TYRE: nucleic acid	
20	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: CDNA	
25	(iii) HYPOTHETICAL: NO	
23	(III) RIPOTABLICAD. NO	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:	
	AGTGGTACCA TCATAATACT CATCCTCCTT C	31
	(2) INFORMATION FOR SEQ 10 NO: 15:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 37 base pairs	
	(B) TYPE: nucleic\acid	
	(C) STRANDEDNESS:\single (D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: CDNA	
	(iii) HYPOTHETICAL: NO	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:	
	CGAAGCTTTA CAAATCTAAT TTCATCACTA AATCGGA	37
50	(2) INFORMATION FOR SEQ ID NO: 16:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 35 base pairs	
55	(B) TYPE: nucleic acid (C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
60	(ii) MOLECULE TYPE: cDNA	
	(iii) HYPOTHETICAL: NO	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO 16:	
65	GCTGCAATAC AAATCTAATT TCATCACTAA ATCGG	35
	No.	

65

	(x) INFORMATION FOR SEQ ID NO: 17:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 876 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO	
15	(iii) ANTI-SENSE: NO (vi) ORIGINAL SOURCE: (A) ORGANISM: Arabidopsis thaliana	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17: ATCATAATAC TCATCCTCCT TCTCAAGGTT CGTACGTATT ATCAATATCT AGTATATACT	60
25	TGTCTTTGTT CTATGCTTTA TATCATCATT TTATGACAAA AAATGATTAA GGTCTTAGTT AATGATTATG TATATGTGAA ACTTATATTT AGGGGCACAA TTTAATTTCG TATGATAATT	120 180
23	GTCTAGTTAG CTTTATGTAC TTATCATAAA AACCTTAGTG TTTATCGCAA TACTTTTCAA	240
2.0	ATATAGTGTA GAATCATAAT GGTCCCACTG TCATTATGTT TGATGCAAAT CTATTTGGAT	300
30	TTTGTTGGAT AATAAACCGA TGACGTGGAC CAGACCAGTA GCTATAAGAT TTGGTTCACA	360
	TAGAAATTTT TTATAAGATA ATGTATCTAG GTTTGCTTAT GATTATACAT GTGATATTTA	420
35	ATACATGGCA CAGGTTCGTC GACTTTCACA GCCATAGGTA CAATAGAAGG CAAATTCGAT	480
	TGTGGTTATC TGGTAAAAGT TAAGTTGGGC TCAGAGATTC TTAACGGCGT TCTTTATCAT	540
40	TCGGCCCAGC CCGCCCATC ATCATCTCCA ACCGCTGTTC TAAACAATGC CGTTGTACCT	600
	TATGTTGAAA CTGGGAGGAG ACGGCGTCGT TTAGGTAAAA GACGAAGAAG CAGACGCAGA	660
45	GAAGATCCGA ATTACCCGAA ACCGAACCGG AGCGGTTACA ATTTCTTCTT TGCTGAGAAA CATTGCAAGC TCAAATCACT TTATCCCAAC AAGGAGAGA AGTTTACGAA ACTTATCGGA	720 780
45	GAATCGTGGA GCAATCTCTC TACCGAAGAA CGAATGGTAA CAAATTATCT TTTAAACCGT	840
	TACCGATTTA GTGATGAAAT TAGATTTGTA GTAAAT	876
50	(2) INFORMATION FOR SEQ ID NO: 18:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1357 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
60	(ii) MOLECULE TYPE: DNA (genomic)	
30	(iii) HYPOTHETICAL: NO	
	(iii) ANTI-SENSE: NO	

7

GTCTTGTACA AATCTAATTT CATCACTAAA TCGG

WO 99/31258 PCT/EP98/08162

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:	
	GGATCCCGG GTACCATCAT AATACTCATC CTCCTTCTCA AGGTTCGTAC GTATTATCAA	60
5	TATCTAGTAT ATACTTGTCT TTGTTCTATG CTTTATATCA TCATTTTATG ACAAAAAATG	120
	ATTAAGGTC TAGTTAATGA TTATGTATAT GTGAAACTTA TATTTAGGGG CACAGTTTAA	180
••	TTTCGTATGA TAATTGTCTA GTTAGCTTTA TGTACTTATC ATAAAAACCT TAGTGTTTAT	240
10	CGCAATACTT TACAAATATA GTGTAGAATC ATAATGGTCC CACTGTCATT ATGTTTGATG	300
	CAAATCTATT TGGATTATAA ACCGATGACG TGGACCAGAC CAGTAGCTAT	360
15	AAGATTTGGT TCACATAGAA ATTTTTTATA AGATAATGTA TCTAGGTTTG CTTATGATTA	420
	TACATGTGAT ATTTAATACA TGGCACAGGT TCGTCGAGTT TCACAGCCAT AGGTACAATA	480
20	GAAGGCAAAT TCGATTGTGG TTATCTGGTA AAAGTTAAGT TGGGCTCAGA GATTCTTAAC	540
20	GGCGTTCTTT ATCATTCGGC CCAGCCCGGC CCATCATCAT CTCCAACCGC TGTTCTAAAC	600
	AATGCCGTTG TACCTTATGT TGAAACTGGG AGGAGACGGC GTCGTTTAGG TAAAAGACGA	660
25	AGAAGCAGAC GCAGAGAGA TCCGAATTAC CCGAAACCGA ACCGGAGCGG TTACAATTTC	720
	TTCTTTGCTG AGAAACATTG CAGCTCAAA TCACTTTATC CCAACAAGGA GAGAGAGTTT	780
30	ACGAAACTTA TCGGAGAATC GTGGAGCAAT CTCTCTACCG AAGAACGAAT GGTAACAAAT	840
	TATCTTTTAA ACCGTTACCG ATTTAGTGAT GAAATTAGAT TTGTATTGCA GCGATTTCAT	900
	TTTAGATTCT CAAAAATATT CTCAGATGTG TGGGATTTGA GTAGAGTTTA TGTTGCGTTG	960
35	GCATGATTTG AATAGTATGC AAGATTTTTG AGATTTTGCA TTCGTTCATG TGTGTATGTG	1020
	TGATTGTAGC TTGATATGAT TTAACCT TT AGTTAAATGT GCATAGACAA TAAGTAACAT	1080
40	ACGAAGCGAG TCACTAAGCA TAAGAGTCAA CTTGTTTTGC TGAAAAGATA TCACTTATGA	1140
	TTTTCGAATC ATTTTAGCTT TTTTGTCACT TGAGCTTAAT GATTCTTCTG AAATTCGATT	1200
	CTTTGTTTGG TTTATGTCAC ATTCTTTAGA ATTGAGAATC TAAGAAATGC TTACAGGATA	1260
45	TGGTGAAACT ATTCTTTTAA GATAGCATGA TGCTTCTTTT ATGATTCTAC AGTGGCTAAG	1320
	TCATTTTTT TTTGTTCTAT TCTTTGTAGC ACCATGG	1357
50	(2) INFORMATION FOR SEQ ID NO: 19:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 34 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: single	
55	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
60	(iii) HYPOTHETICAL: NO	
	(will province propression, SEO ID NO. 19.	

		(
	5	
	10	
	15	T
	20	(
there there is a	25	
الله الله الله الله الله الله الله الله	30	
an Hine Court in	35	•
The first the state of the stat	40	
	45	
	50	
	55	

	(2) INFORMATION FOR SEQ ID NO: 20:	
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 34 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
10	(ii) NOLECULE TYPE: CDNA (iii) HYPOTHETICAL: NO	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:	
	TTAGATTTGT ACAAGACCCT TCCTCTATAT AAGG	34
20	(2) INFORMATION FOR SEQ ID NO: 21:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 base pairs (B) TYPE: nucleic acid (C) STRANGEDNESS: single 	
25	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
30	(iii) HYPOTHETICAL:\NO	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:	
35	TTCCCAGTCA CGACGTTGT	19
	(2) INFORMATION FOR SEQ ID NO: 22:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1006 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: DNA (genomic)	
	(iii) HYPOTHETICAL: NO	
	(iii) ANTI-SENSE: NO	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:	
55	GGATCCCCGG GTACCATCAT AATACTCATC TCCTTCTCA AGGTTCGTAC GTATTATCAA	60
	TATCTAGTAT ATACTTGTCT TTGTTCTATG CTTTATATCA TCATTTTATG ACAAAAAATG	120
60	ATTAAGGTCT TAGTTAATGA TTATGTATAT GTGAAACTTA TATTTAGGGG CACAGTTTAA	180
	TTTCGTATGA TAATTGTCTA GTTAGCTTTA TGTACTTATC ATAAAAACCT TAGTGTTTAT	240
	CGCAATACTT TTCAAATATA GTGTAGAATC ATAATGGTCC CACTGTCATT ATGTTTGATG	300
65	CAAATCTATT TGGATTTTGT TGGATAATAA CCCGATGACG TGGACCAGAC CAGTAGCTAT	360

WO 99/31258

	AAGATTTGGT	TCACATAGAA	ATTTTTTATA	AGATAATGTA	TCTAGGTTTG	CTTATGATTA	420
5	TACATGTGAT	ATTTATACA	TGGCACAGGT	TCGTCGAGTT	TCACAGCCAT	AGGTACAATA	480
3	GAAGGCAAAT	TCGATTCTGG	TTATCTGGTA	AAAGTTAAGT	TGGGCTCAGA	GATTCTTAAC	540
	GGCGTTCTTT	ATCATTCGOC	CCAGCCCGGC	CCATCATCAT	CTCCAACCGC	TGTTCTAAAC	600
10	AATGCCGTTG	TACCTTATGT	TGAAACTGGG	AGGAGACGGC	GTCGTTTAGG	TAAAAGACGA	660
	AGAAGCAGAC	GCAGAGAAGA	TOCGAATTAC	CCGAAACCGA	ACCGGAGCGG	TTACAATTTC	720
15	TTCTTTGCTG	AGAAACATTG	CAAGCTCAAA	TCACTTTATC	CCAACAAGGA	GAGAGAGTTT	780
13	ACGAAACTTA	TCGGAGAATC	GTGGACCAAT	CTCTCTACCG	AAGAACGAAT	GGTAACAAAT	840
	TATCTTTTAA	ACCGTTACCG	ATTTAGTGAT	GAAATTAGAT	TTGTACAAGA	CCCTTCCTCT	900
20	ATATAAGGAA	GTTCATTTCA	TTTGGAGAG	ACACGTATTT	TTACAACAAT	TACCAACAAC	960
	AACAAACAAC	AAACAACATT	ACAATTACTA	TTTACAATTA	CCATGG		1006

PCT/EP98/08162